

AMENDMENTS TO THE CLAIMS:

Please amend the claims as follows:

1. (Currently Amended) ~~A method~~ Method for increasing plant yield relative to a corresponding wild type plant[[s]], comprising increasing ~~modifying~~ expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein ~~and/or modifying in a plant level and/or activity of a 2xC2H2 zinc finger protein~~, said 2xC2H2 zinc finger protein comprising a motif having at least 80% identity to any one or more of the motifs selected from the group consisting of :

(i) SEQ ID NO 5, wherein the Leu at position 3 may be any hydrophobic amino acid;

(ii) SEQ ID NO 7 wherein Xaa at positions 1 and 5 is any hydrophobic residue and Xaa at position 6 is optionally present and, when present, is any amino acid;

(iii) SEQ ID NO 8 wherein the Ser at position 3 is optionally present;

(iv) SEQ ID NO 9 wherein each Xaa is independently any amino acid; and

(v) a motif according to (i) to (iv) further containing at least one conserved amino acid substitution; and

selecting a plant having increased yield as compared to a corresponding wild type plant.

2. (Currently Amended) ~~A method~~ Method for increasing leaf surface area relative to a corresponding wild type plant[[s]], comprising increasing ~~modifying~~ expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein,

said 2xC2H2 zinc finger protein comprising a motif having at least 80% identity to any one or more of the motifs selected from the group consisting of :

(i) SEQ ID NO 5, wherein the Leu at position 3 may be any hydrophobic amino acid;

(ii) SEQ ID NO 7 wherein Xaa at positions 1 and 5 is any hydrophobic residue and Xaa at position 6 is optionally present and, when present, is any amino acid;

(iii) SEQ ID NO 8 wherein the Ser at position 3 is optionally present;

(iv) SEQ ID NO 9 wherein each Xaa is independently any amino acid; and

(v) a motif according to (i) to (iv) further containing at least one conserved amino acid substitution and/or modifying in a plant level and/or activity of a 2xC2H2 zinc finger protein.

3. (Currently Amended) ~~A method~~ Method for prolonging vegetative growth phase of a plant relative to a corresponding wild type plant[[s]], comprising increasing ~~modifying~~ expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein, said 2xC2H2 zinc finger protein comprising a motif having at least 80% identity to any one or more of the motifs selected from the group consisting of :

(i) SEQ ID NO 5, wherein the Leu at position 3 may be any hydrophobic amino acid;

(ii) SEQ ID NO 7 wherein Xaa at positions 1 and 5 is any hydrophobic residue and Xaa at position 6 is optionally present and, when present, is any amino acid;

(iii) SEQ ID NO 8 wherein the Ser at position 3 is optionally present;

(iv) SEQ ID NO 9 wherein each Xaa is independently any amino acid; and

(v) a motif according to (i) to (iv) further containing at least one conserved amino acid substitution and/or modifying in a plant level and/or activity of a 2xC2H2 zinc-finger protein.

4. (Currently Amended) A method ~~Method~~ according to claim 1, wherein said ~~modifying increasing~~ expression, ~~level and/or activity~~ is effected by recombinant means ~~and/or chemical means~~.

Claim 5. (Canceled)

Claim 6. (Canceled)

Claim 7. (Canceled)

Claim 8. (Canceled)

Claim 9. (Canceled)

10. (Previously Presented) A method ~~Method~~ according to claim 1, wherein said 2xC2H2 zinc finger protein is ~~derived from a~~ dicotyledonous plant 2xC2H2 zinc finger protein, ~~preferably from the family Brassicaceae, further preferably from Arabidopsis thaliana, more preferably the nucleic acid is as represented by SEQ ID NO 2 or a homologue, derivative or active fragment thereof and/or wherein said nucleic acid is as represented by SEQ ID NO 4 or a portion thereof or sequences capable of hybridising therewith.~~

11. (Currently Amended) A method ~~Method~~ according to claim [[10]]46, wherein said homologue, derivative or active fragment has, ~~in increasing order of preference,~~ at least 30%, ~~31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 52%, 54%, 56%, 58%, 60%, 62%, 64%, 66%, 68%, 70%, 72%, 74%, 76%, 78%, 80%, 82%, 84%, 86%, 88%, 90%, 92%, 94%, 96%, 98%~~ sequence identity with the sequence of SEQ ID NO 2.

12. (Currently Amended) A method ~~Method~~ according to claim 1, wherein said plant is a monocot.

13. (Currently Amended) A method ~~Method~~ according to claim 1, wherein said ~~increasing~~ modifying expression is effected by introducing into [[a]]~~the~~ plant a nucleic acid capable of ~~increasing~~ modifying expression of a gene encoding [[a]]~~said~~ 2xC2H2 zinc finger protein ~~and/or capable of modifying level and/or activity of a 2xC2H2 zinc finger protein.~~

14. (Currently Amended) A method ~~Method~~ according to claim 13, wherein said nucleic acid capable of ~~increasing~~ modifying expression is a nucleic acid encoding [[a]]~~said~~ 2xC2H2 protein, ~~such as a 2xC2H2 protein.~~

15. (Currently Amended) A method ~~Method~~ according to claim 13, wherein said nucleic acid introduced into [[a]]~~the~~ plant is an alternative splice variant of the of [[a]]~~the~~ nucleic acid encoding a 2xC2H2 zinc finger protein.

16. (Currently Amended) A method ~~Method~~ according to claim 13, wherein said nucleic acid introduced into ~~[[a]]the~~ plant is an allelic variant of the of ~~[[a]]the~~ nucleic acid encoding a 2xC2H2 zinc finger protein.

17. (Currently Amended) A method ~~Method~~ according to claim 13, wherein said nucleic acid introduced into ~~[[a]]the~~ plant is comprised on at least part of a chromosome.

Claim 18. (Canceled)

19. (Currently Amended) A method ~~Method~~ according to claim 1, wherein expression of said nucleic acid is driven by a plant promoter, ~~preferably a constitutive promoter, such as a GOS2 promoter.~~

20. (Currently Amended) A method ~~Method~~ according to claim ~~[[1]]19~~, wherein ~~the expression of said nucleic acid is driven by a plant promoter, preferably is a tissue preferred promoter, such as seed preferred promoter.~~

21. (Currently Amended) A method ~~Method~~ according to claim 1, wherein said increased yield comprises increased above ground biomass.

22. (Currently Amended) A method ~~Method~~ according to claim 1, wherein said increased yield comprises increased seed yield.

23. (Currently Amended) A method ~~Method~~ according to claim 1, wherein said increased yield comprises increased root yield.

Claim 24. (Canceled)

Claim 25. (Canceled)

Claim 26. (Canceled)

Claim 27. (Canceled)

Claim 28. (Canceled)

29. (Currently Amended) A method ~~Method~~ for the production of a transgenic plant having increased yield, increased leaf surface area and/or prolonged vegetative growth, which method comprises

(i) introducing into a plant or plant cell a nucleic acid sequence encoding a 2xC₂H₂ zinc finger protein, said 2xC₂H₂ zinc finger protein comprising a motif having at least 80% identity to any one or more of the motifs selected from the group consisting of
:

(a) SEQ ID NO 5, wherein the Leu at position 3 may be any hydrophobic amino acid;

(b) SEQ ID NO 7 wherein Xaa at positions 1 and 5 is any hydrophobic residue and Xaa at position 6 is optionally present and, when present, is any amino acid;

(c) SEQ ID NO 8 wherein the Ser at position 3 is optionally present;

(d) SEQ ID NO 9 wherein each Xaa is independently any amino acid; and

(e) a motif according to (a) to (d) further containing at least one conserved amino acid substitution a 2xC2H2 zinc finger nucleic acid;

(ii) Cultivating the plant or plant cell under conditions promoting plant growth;
and

(iii) selecting for plants having increased yield.

30. (Currently Amended) A plant ~~Plant~~ obtainable by a method according to claim 1, or a harvestable part of said plant or a propagule of said plant or a progeny of said plant, which plant, part, propagule or progeny has increased yield, modified leaf surface area and/or prolonged vegetative growth, relative to a corresponding wild type plant [[s]], part, propagule or progeny.

31. (Currently Amended) A transgenic ~~Transgenic~~ plant having increased yield, increased leaf surface area and/or prolonged vegetative growth, which transgenic plant has modified expression of a nucleic acid encoding a 2xC2H2 zinc finger protein relative to corresponding wild type plants, said 2xC2H2 zinc finger protein comprising a motif having at least 80% identity to any one or more of the motifs selected from the group consisting of :

- (i) SEQ ID NO 5, the Leu at position 3 may be any hydrophobic amino acid;
- (ii) SEQ ID NO 7 wherein Xaa at positions 1 and 5 is any hydrophobic residue and Xaa at position 6 is optionally present and, when present, is any amino acid;
- (iii) SEQ ID NO 8 wherein the Ser at position 3 is optionally present;
- (iv) SEQ ID NO 9 wherein each Xaa is independently any amino acid; and

(v) a motif according to (i) to (iv) further containing at least one conserved amino acid substitution and/or modified level and/or activity of a 2xC2H2 zinc finger protein, relative to corresponding wild type plants.

32. (Currently Amended) A plant ~~Plant part, preferably a harvestable part, a propagule or progeny of a plant as defined in claim 30, which progeny has modified expression of [[a]]the nucleic acid encoding 2xC2H2 zinc finger protein and/or modified level and/or activity of a 2xC2H2 zinc finger protein, relative to corresponding wild type plants.~~

33. (Currently Amended) A plant ~~Plant or plant part according to claim 30, which plant is a monocotyledonous plant, preferably a cereal.~~

34. (Currently Amended) A plant ~~Plant or plant part according to claim 30 selected from rice, maize, wheat, barley, millet, oats, rye, sorghum, soybean, sunflower, canola, sugarcane, alfalfa, leguminosae (bean, pea), flax, lupinus, rapeseed, tobacco, tomato, potato, squash, papaya, poplar and cotton.~~

Claims 35-42. (Canceled)

43. (new) The method of claim 1 wherein Gln at position 1 of SEQ ID NO:5 of (i) is Gly, Lys or Arg, or Ala at position 2 of SEQ ID NO:5 of (i) is Ser, or Leu at position 3 of SEQ ID NO:5 of (i) is Phe.

44. (new) The method of claim 10 wherein said dicotyledonous plant is from the family Brassicaceae

45. (new) The method of claim 10 wherein said dicotyledonous plant is *Arabidopsis thaliana*.

46. (new) The method of claim 10 wherein said 2xC2H2 zinc finger protein is SEQ ID NO:2 or a homologue, derivative or active fragment thereof.

47. (new) The method of claim 10 wherein said 2xC2H2 zinc finger protein is a protein encoded by SEQ ID NO:1 or a portion of SEQ ID NO:1 or said protein is encoded by a nucleic acid sequences capable of completely hybridizing with SEQ ID NO:1.

48. (new) The method according to claim 46, wherein said homologue, derivative or active fragment has at least 94% sequence identity with the sequence of SEQ ID NO 2.

49. (new) The method according to claim 19, wherein the plant promoter is a constitutive promoter.

50. (new) The method of claim 49, wherein the promoter is a GOS2 promoter.

51. (new) The method according to claim 20, wherein the tissue preferred promoter is a seed-preferred promoter.

52. (new) A plant or plant part according to claim 33, which plant is a cereal.